

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/849,980Bre-run  
DATE: 08/14/2003  
TIME: 15:04:29

INPUT SET: S36789.raw

**This Raw Listing contains the General  
Information Section and up to the first 5 pages.**

## SEQUENCE LISTING

ENTERED

1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: SANTEN PHARMACEUTICAL CO., LTD.  
6 (ii) TITLE OF INVENTION: Novel Polypeptide Having Water Channel  
7 Activity and DNA sequence  
8 (iii) NUMBER OF SEQUENCES: 2  
9 (iv) CORRESPONDENCE ADDRESS:  
10 (A) ADDRESSEE: SANTEN PHARMACEUTICAL CO., LTD.  
11 (B) STREET: 9 19 Shimoshinjo 3-chome Higashiyodogawa-Ku  
12 (C) CITY: Osaka  
13 (D) STATE: Osaka  
14 (E) COUNTRY: JAPAN  
15 (F) ZIP: 533-0021  
16 (v) COMPUTER READABLE FORM:  
17 (A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB, storage  
18 (B) COMPUTER: IBM PS/2 or compatibles  
19 (C) OPERATING SYSTEM: WINDOWS 95/97  
20 (D) SOFTWARE: Microsoft Word 97  
21 (vi) CURRENT APPLICATION DATA:  
22 (A) APPLICATION NUMBER: US/09/849,980B  
23 (B) FILING DATE: 19-OCT-1999  
24 (C) CLASSIFICATION:  
25 (vii) PRIOR APPLICATION DATA:  
26 (A) APPLICATION NUMBER: PCT/JP98/01371  
27 (B) FILING DATE: 27-MAR-1998  
28 (C) APPLICATION NUMBER: JP 09-094845  
29 (D) FILING DATE: 28-MAR-1997  
30 (viii) ATTORNEY/AGENT INFORMATION:  
31 (A) NAME: Burton A. Amernick  
32 (B) REGISTRATION NUMBER: 24852  
33 (C) REFERENCE/DOCKET NUMBER: 1581/00156  
34 (ix) TELECOMMUNICATION INFORMATION:  
35 (A) TELEPHONE: (202)331-7111  
36 (B) TELEFAX: (202)293-6229  
37  
38 (2) INFORMATION FOR SEQ ID NO: 1:  
39  
40 (i) SEQUENCE CHARACTERISTICS:  
41 (A) LENGTH: 342 amino acids  
42 (B) TYPE: amino acid  
43 (D) TOPOLOGY: linear  
44 (ii) MOLECULE TYPE: peptide  
45  
46 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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47
48 Met Val Gln Ala Ser Gly His Arg Arg Ser Thr Arg Gly Ser Lys Met
49                               5                               10                               15
50 Val Ser Trp Ser Val Ile Ala Lys Ile Gln Glu Ile Leu Gln Arg Lys
51                               20                               25                               30
52 Met Val Arg Glu Phe Leu Ala Glu Phe Met Ser Thr Tyr Val Met Met
53                               35                               40                               45
54 Val Phe Gly Leu Gly Ser Val Ala His Met Val Leu Asn Lys Lys Tyr
55                               50                               55                               60
56 Gly Ser Tyr Leu Gly Val Asn Leu Gly Phe Gly Phe Gly Val Thr Met
57                               65                               70                               75                               80
58 Gly Val His Val Ala Gly Arg Ile Ser Gly Ala His Met Asn Ala Ala
59                               85                               90                               95
60 Val Thr Phe Ala Asn Cys Ala Leu Gly Arg Val Pro Trp Arg Lys Phe
61                               100                              105                              110
62 Pro Val Tyr Val Leu Gly Gln Phe Leu Gly Ser Phe Leu Ala Ala Ala
63                               115                              120                              125
64 Thr Ile Tyr Ser Leu Phe Tyr Thr Ala Ile Leu His Phe Ser Gly Gly
65                               130                              135                              140
66 Gln Leu Met Val Thr Gly Pro Val Ala Thr Ala Gly Ile Phe Ala Thr
67                               145                              150                              155                              160
68 Tyr Leu Pro Asp His Met Thr Leu Trp Arg Gly Phe Leu Asn Glu Ala
69                               165                              170                              175
70 Trp Leu Thr Gly Met Leu Gln Leu Cys Leu Phe Ala Thr Thr Asp Gln
71                               180                              185                              190
72 Glu Asn Asn Pro Ala Leu Pro Gly Thr Glu Ala Leu Val Ile Gly Ile
73                               195                              200                              205
74 Leu Val Val Ile Ile Gly Val Ser Leu Gly Met Asn Thr Gly Tyr Ala
75                               210                              215                              220
76 Ile Asn Pro Ser Arg Asp Leu Pro Pro Arg Ile Phe Thr Phe Ile Ala
77                               225                              230                              235                              240
78 Gly Trp Gly Lys Gln Val Phe Ser Asn Gly Glu Asn Trp Trp Trp Val
79                               245                              250                              255
80 Pro Val Val Ala Pro Leu Leu Gly Ala Tyr Leu Gly Gly Ile Ile Tyr
81                               260                              265                              270
82 Leu Val Phe Ile Gly Ser Thr Ile Pro Arg Glu Pro Leu Lys Leu Glu
83                               275                              280                              285
84 Asp Ser Val Ala Tyr Glu Asp His Gly Ile Thr Val Leu Pro Lys Met
85                               290                              295                              300
86 Gly Ser His Glu Pro Thr Ile Ser Pro Leu Thr Pro Val Ser Val Ser
87                               305                              310                              315                              320
88 Pro Ala Asn Arg Ser Ser Val His Pro Ala Pro Pro Leu His Glu Ser
89                               325                              330                              335
90 Met Ala Leu Glu His Phe
91                               340
92
93 (2) INFORMATION FOR SEQ ID NO:2:
94 (i) SEQUENCE CHARACTERISTICS:
95 (A) LENGTH:1258 base pairs
96 (B) TYPE: nucleic acid
97 (C) STRANDEDNESS: double
98 (D) TOPOLOGY: linear
99 (ii) MOLECULE TYPE: cDNA to mRNA

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100 (vi) ORIGINAL SOURCE:
101 (A) ORGANISM: Homo sapiens
102 (B) TISSUE TYPE: fat tissue
103 (ix) FEATURE:
104 (A) NAME/KEY: exon
105 (B) LOCATION: F173..1198
106 (C) IDENTIFICATION METHOD: by experiment
107 (C) IDENTIFICATION METHOD: by experiment
108 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
109
110 GGCTCTGGAC TGGGGACACA GGGATAGCTG AGCCCCAGCT GGGGGTGGAA GCTGAGCCAG 60
111 GGACAGTCAC GGAGGAACAA GATCAAGATG CGCTGTAAC TACAAGCCCC CAAGGCGGAG 120
112 GCTGAGAATC AGAGACATTT CAGCAGACAT CTACAAATCT GAAAGACAAA AC ATG GTT 178
113 Met Val
114 1
115 CAA GCA TCC GGG CAC AGG CGG TCC ACC CGT GGC TCC AAA ATG GTC TCC 226
116 Gln Ala Ser Gly His Arg Arg Ser Thr Arg Gly Ser Lys Met Val Ser
117 5 10 15
118 TGG TCC GTG ATA GCA AAG ATC CAG GAA ATA CTG CAG AGG AAG ATG GTG 274
119 Trp Ser Val Ile Ala Lys Ile Gln Glu Ile Leu Gln Arg Lys Met Val
120 20 25 30
121 CGA GAG TTC CTG GCC GAG TTC ATG AGC ACA TAT GTC ATG ATG GTA TTC 322
122 Arg Glu Phe Leu Ala Glu Phe Met Ser Thr Tyr Val Met Met Val Phe
123 35 40 45 50
124 GGC CTT GGT TCC GTG GCC CAT ATG GTT CTA AAT AAA AAA TAT GGG AGC 370
125 Gly Leu Gly Ser Val Ala His Met Val Leu Asn Lys Lys Tyr Gly Ser
126 55 60 65
127 TAC CTT GGT GTC AAC TTG GGT TTT GGC TTC GGA GTC ACC ATG GGA GTG 418
128 Tyr Leu Gly Val Asn Leu Gly Phe Gly Phe Gly Val Thr Met Gly Val
129 70 75 80
130 CAC GTG GCA GGC CGC ATC TCT GGA GCC CAC ATG AAC GCA GCT GTG ACC 466
131 His Val Ala Gly Arg Ile Ser Gly Ala His Met Asn Ala Ala Val Thr
132 85 90 95
133 TTT GCT AAC TGT GCG CTG GGC CGC GTG CCC TGG AGG AAG TTT CCG GTC 514
134 Phe Ala Asn Cys Ala Leu Gly Arg Val Pro Trp Arg Lys Phe Pro Val
135 100 105 110
136 TAT GTG CTG GGG CAG TTC CTG GGC TCC TTC CTG GCG GCT GCC ACC ATC 562
137 Tyr Val Leu Gly Gln Phe Leu Gly Ser Phe Leu Ala Ala Ala Thr Ile
138 115 120 125 130
139 TAC AGT CTC TTC TAC ACG GCC ATT CTC CAC TTT TCG GGT GGA CAG CTG 610
140 Tyr Ser Leu Phe Tyr Thr Ala Ile Leu His Phe Ser Gly Gly Gln Leu
141 135 140 145
142 ATG GTG ACC GGT CCC GTC GCT ACA GCT GGC ATT TTT GCC ACC TAC CTT 658
143 Met Val Thr Gly Pro Val Ala Thr Ala Gly Ile Phe Ala Thr Tyr Leu
144 150 155 160
145 CCT GAT CAC ATG ACA TTG TGG CGG GGC TTC CTG AAT GAG GCG TGG CTG 706
146 Pro Asp His Met Thr Leu Trp Arg Gly Phe Leu Asn Glu Ala Trp Leu
147 165 170 175
148 ACC GGG ATG CTC CAG CTG TGT CTC TTC GCC ATC ACG GAC CAG GAG AAC 754
149 Thr Gly Met Leu Gln Leu Cys Leu Phe Ala Thr Thr Asp Gln Glu Asn
150 180 185 190
151 AAC CCA GCA CTG CCA GGA ACA GAG GCG CTG GTG ATA GGC ATC CTC GTG 802
152 Asn Pro Ala Leu Pro Gly Thr Glu Ala Leu Val Ile Gly Ile Leu Val

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153	195	200	205	210	
154	GTC ATC ATC GGG GTG TCC CTT GGC ATG AAC ACA GGA TAT GCC ATC AAC	850			
155	Val Ile Ile Gly Val Ser Leu Gly Met Asn Thr Gly Tyr Ala Ile Asn				
156	215 220 225				
157	CCG TCC CGG GAC CTG CCC CCC CGC ATC TTC ACC TTC ATT GCT GGT TGG	898			
158	Pro Ser Arg Asp Leu Pro Pro Arg Ile Phe Thr Phe Ile Ala Gly Trp				
159	230 235 240				
160	GGC AAA CAG GTC TTC AGC AAT GGG GAG AAC TGG TGG TGG GTG CCA GTG	946			
161	Gly Lys Gln Val Phe Ser Asn Gly Glu Asn Trp Trp Trp Val Pro Val				
162	245 250 255				
163	GTG GCA CCA CTT CTG GGT GCC TAT CTA GGT GGC ATC ATC TAC CTG GTC	994			
164	Val Ala Pro Leu Leu Gly Ala Tyr Leu Gly Gly Ile Ile Tyr Leu Val				
165	260 265 270				
166	TTC ATT GGC TCC ACC ATC CCA CGG GAG CCC CTG AAA TTG GAG GAT TCT	1042			
167	Phe Ile Gly Ser Thr Ile Pro Arg Glu Pro Leu Lys Leu Glu Asp Ser				
168	275 280 285 290				
169	GTG GCG TAT GAA GAC CAC GGG ATA ACC GTA TTG CCC AAG ATG GGA TCT	1090			
170	Val Ala Tyr Glu Asp His Gly Ile Thr Val Leu Pro Lys Met Gly Ser				
171	295 300 305				
172	CAT GAA CCC ACG ATC TCT CCC CTC ACC CCC GTC TCT GTG AGC CCT GCC	1138			
173	His Glu Pro Thr Ile Ser Pro Leu Thr Pro Val Ser Val Ser Pro Ala				
174	310 315 320				
175	AAC AGA TCT TCA GTC CAC CCT GCC CCA CCC TTA CAT GAA TCC ATG GCC	1186			
176	Asn Arg Ser Ser Val His Pro Ala Pro Pro Leu His Glu Ser Met Ala				
177	325 330 335				
178	CTA GAG CAC TTC TAAGCAGAGA TTATTTGTGA TCCCATCCAT TCCCCAATAA	1238			
179	Leu Glu His Phe				
180	340				
181	AGCAAGGCTT GTCCGACAAA	1258			
182					
183					

PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/849,980B**

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Line	Error	Original Text
22	Wrong application Serial Number	(A) APPLICATION NUMBER:US/09/849,980B